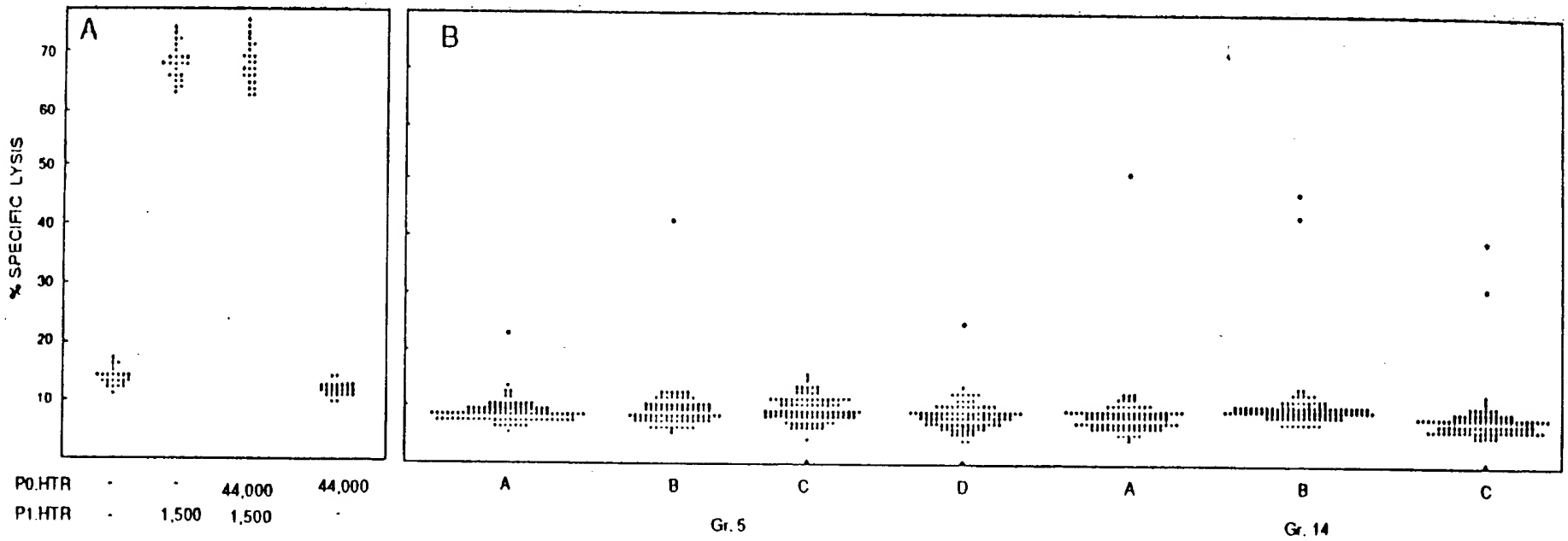


Figure 1

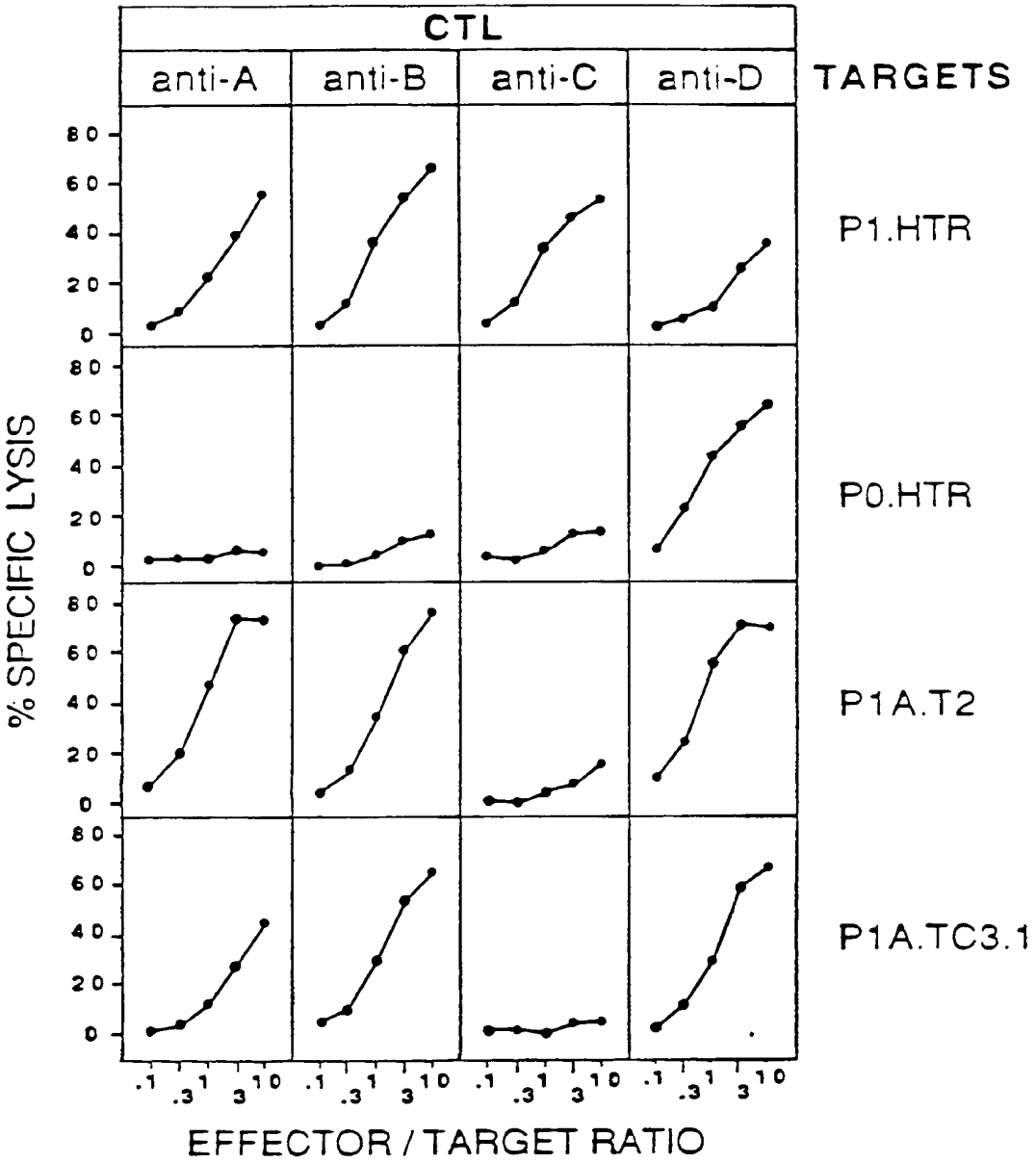
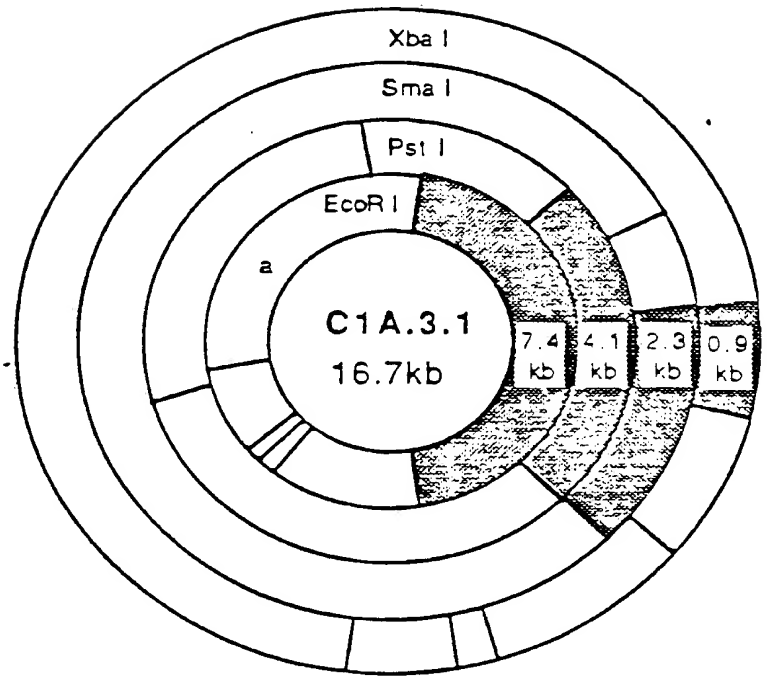

CTL
anti-A
anti-B
anti-C
anti-D
TARGETS
P1.HTR
P0.HTR
P1A.T2
P1A.TC3.1
% SPECIFIC LYSIS
0
20
40
60
80
.1
.3
1
3
10
EFFECTOR / TARGET RATIO

Figure 2



Transfection of restriction fragments

	No. of clones expressing P815A / no. of HmB^r clones
4.1 kb Pst I - Pst I	2/16
2.3 kb Sma I -Pst I	16/96
0.9 kb Sma I - Xba I	22/96

Figure 3

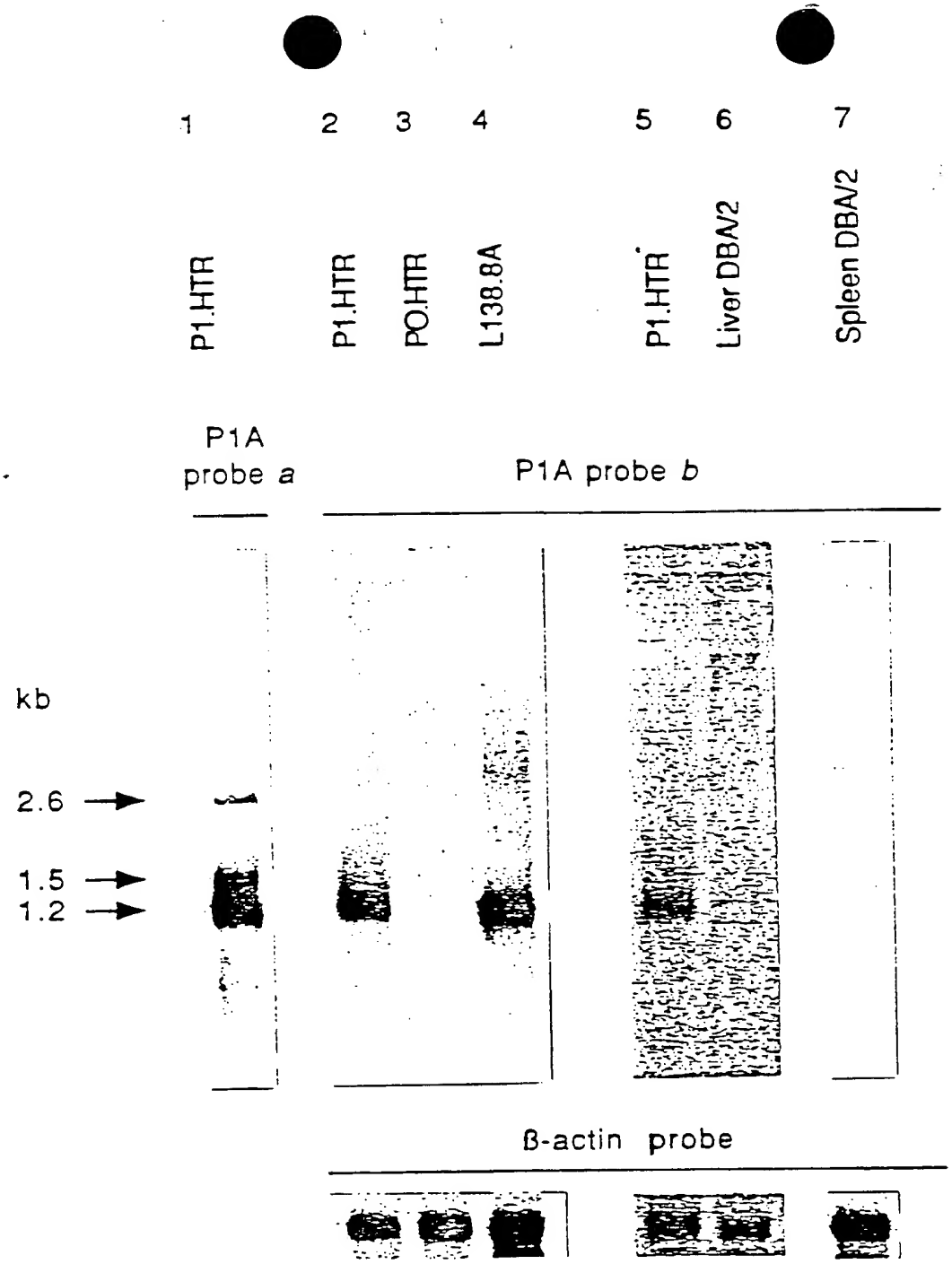

1
2
3
4
5
6
7
P1.HTR
P1.HTR
PO.HTR
L138.8A
P1.HTR
Liver DBA/2
Spleen DBA/2
P1A probe a
P1A probe b
kb
2.6
1.5
1.2
ß-actin probe

Figure 4

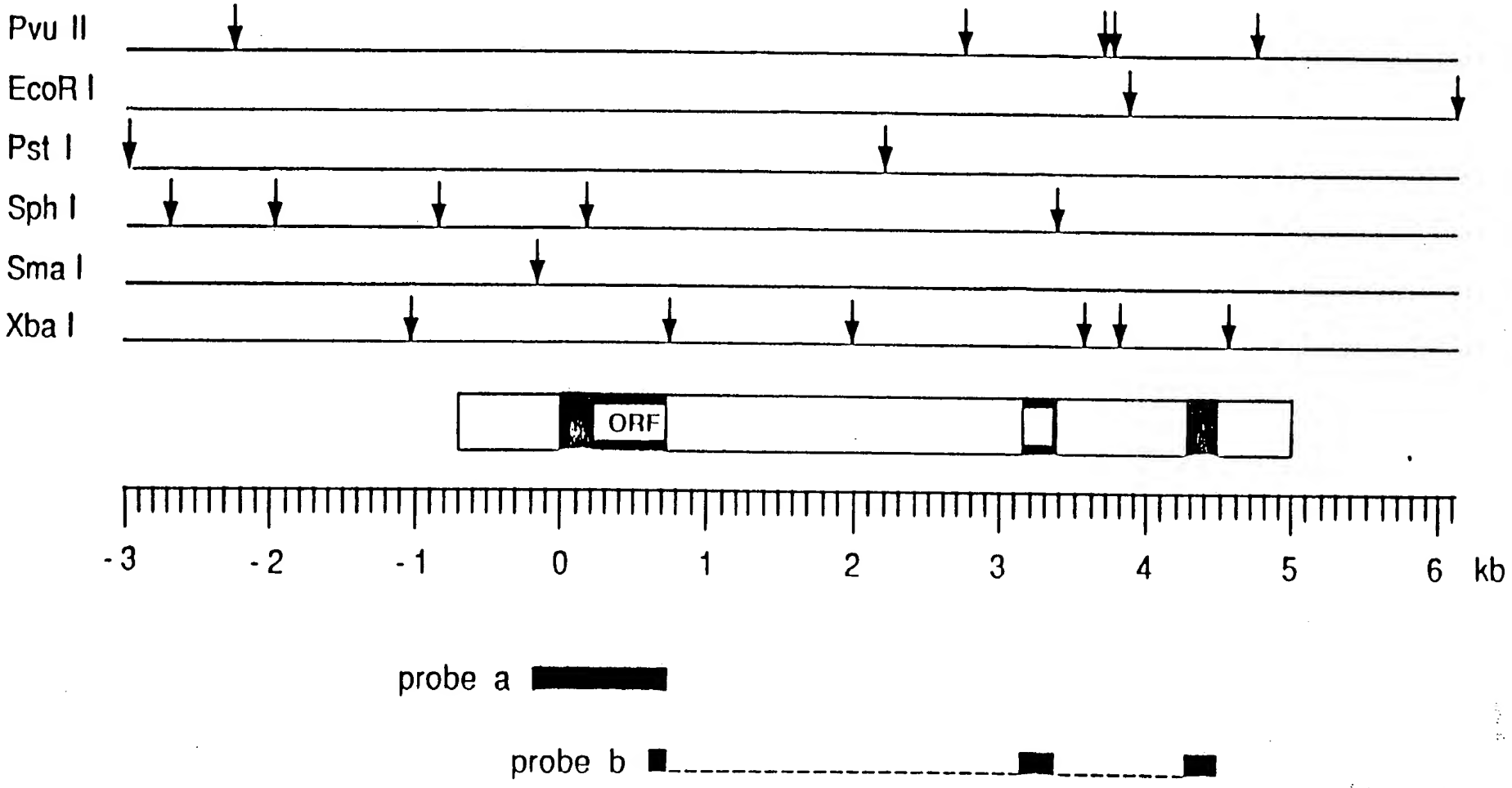


Figure 5

```
ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG ATCACTCATT   -120
GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC   -50
CTTGGGTAGG AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT CACGTAAAAA    19
AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC    89
CTTATAGAAG TCTTCCGTAT AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG   159
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT   229
TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC  271
```

FIGURE 6a

```
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT GAC GGT GAT GGG  59
Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly Asp Gly Asp Gly

AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG  118
Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu Glu Ile Leu Pro Tyr Leu Gly Trp

CTG GTC TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT  177
Leu Val Phe Ala Val Val Thr Thr Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu

TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC  236
Tyr Glu Glu Gln Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser

TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC GAG GAC  295
Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr Asp Asp Glu Asp

GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT GAG GAA GAA GAA TTG GAG AAC CTG  354
Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp Glu Glu Glu Glu Leu Glu Asn Leu

ATG GAT GAT GAA TCA GAA GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA  413
Met Asp Asp Glu Ser Glu Asp Glu Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly

GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG  472
Ala Glu Glu Met Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys

AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA  531
Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe Leu Val Ser Ile

CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT GAA GAG GTT GCA  590
Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys Glu Asn Ala Asp Glu Glu Val Ala

ATG GAA GAG GAA GAA GAA GAA GAG GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT  649
Met Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp

GGC TTC TCA CCT TAG

Gly Phe Ser Pro Amb
```

FIGURE 6b

```
GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT   60

TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT  120

TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACTTT CATATGATAC  180

ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC               228
```

FIGURE 6c

cDNA Sequence of gene P1A
Content of ASCII file : CDNA (cfr Figure 6, parts a,b & c)

```
ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT
GAAGATCCTG ATCACTCATT GGGTGTCTCA GTTCTGCGAT ATTCATCCCT
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT
ACAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGCTCGAAG AAGTAAGCCG
CTACCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT
ACCCTTTGTG CC
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAC ATG TTC
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT CAG
GAT GAA GAC GAT GAC GAT GAT GAG GAT GAC TAC TAC GAC GAC
GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATC GGT CCC GGA
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT
GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT
TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG
AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT
GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG GAG GAG
GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT
TAG
GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG
TTGTTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA
ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT
CTGACTGCAT GGTGAACTTT CATATGATAC ATACCATTAC ACTTGTACCT
GTTAAAAATA AAAGTTTGAC TTGCATAC
```

Figure 6d

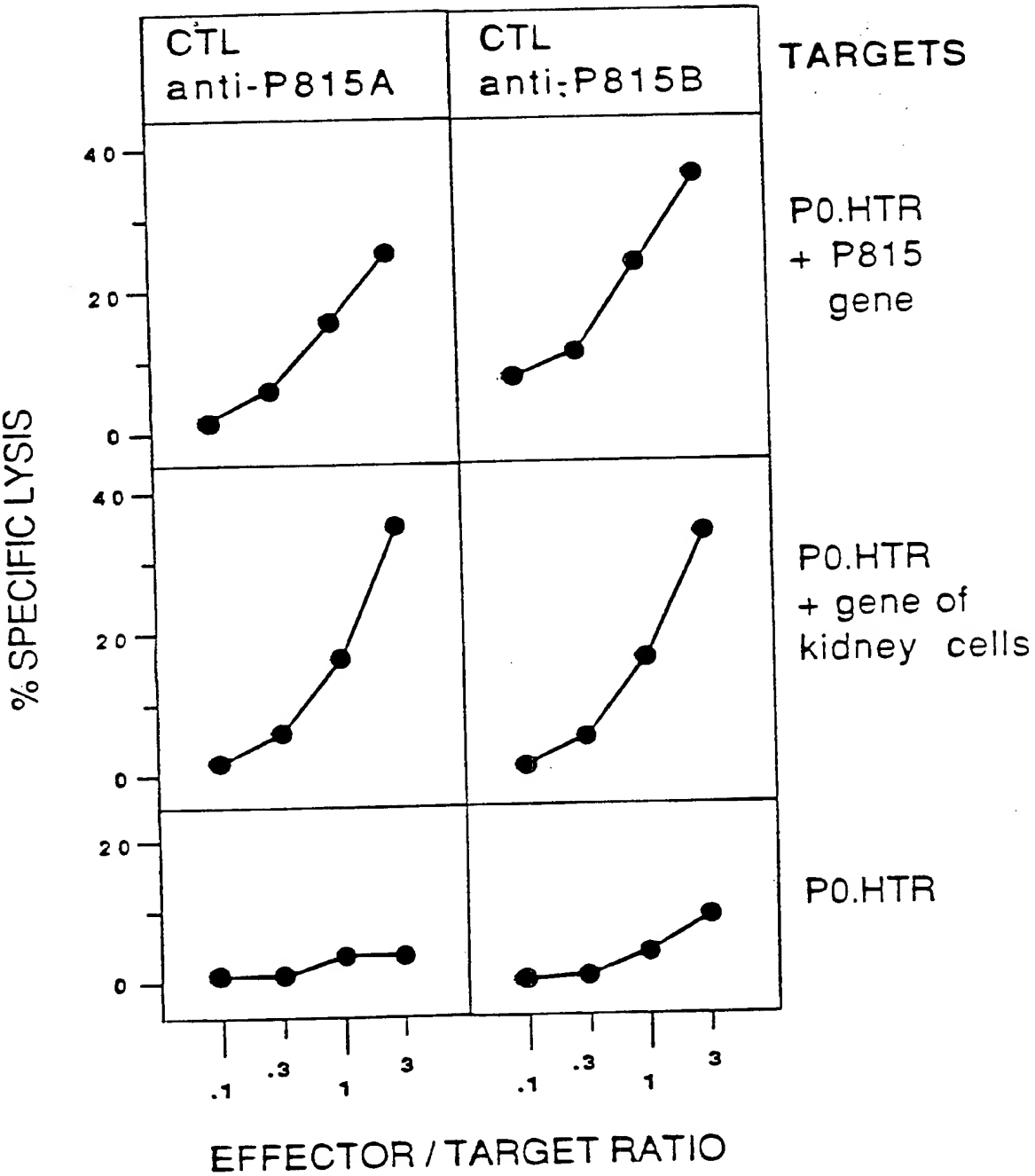

CTL anti-P815A
CTL anti-P815B
TARGETS
P0.HTR + P815 gene
P0.HTR + gene of kidney cells
P0.HTR
% SPECIFIC LYSIS
40
20
0
.1
.3
1
3
EFFECTOR / TARGET RATIO

Figure 7

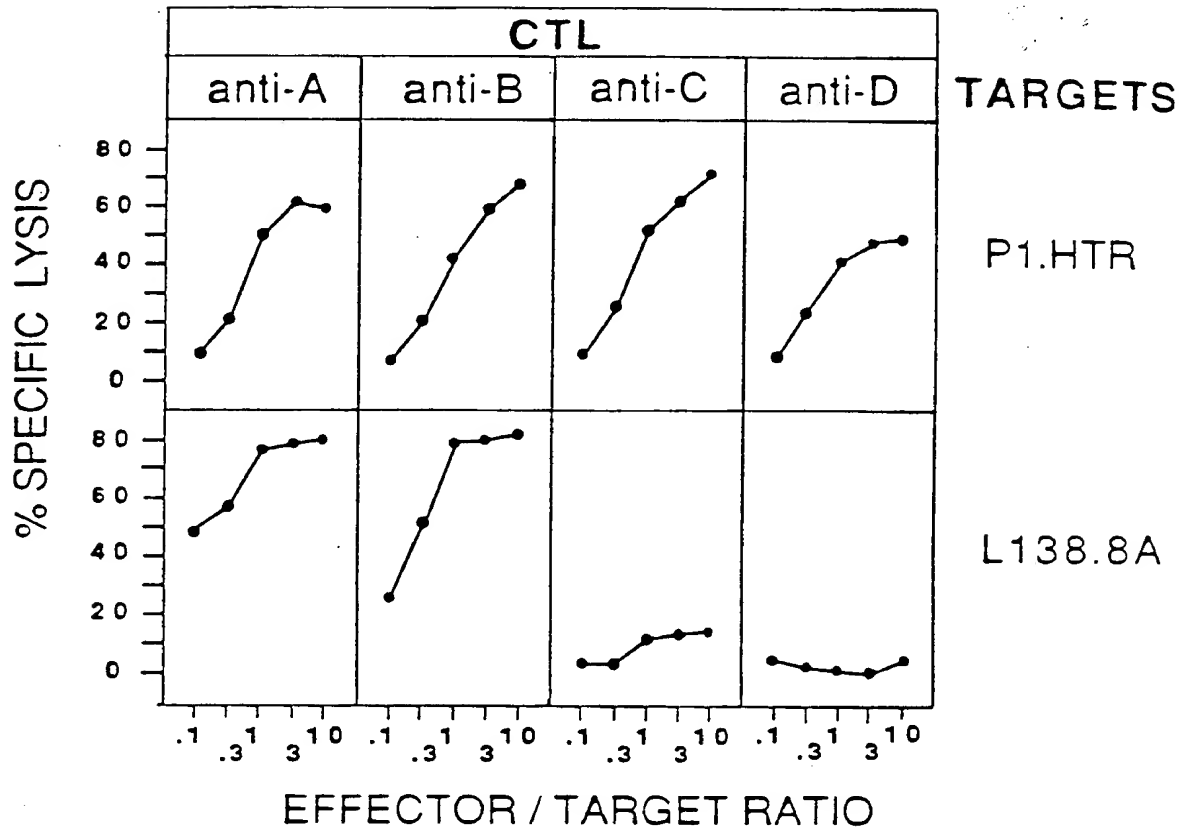

CTL
anti-A
anti-B
anti-C
anti-D
TARGETS
P1.HTR
L138.8A
% SPECIFIC LYSIS
0
20
40
60
80
.1
.3
1
3
10
EFFECTOR / TARGET RATIO

Figure 8

Genomic Sequence of gene P1A
Content of ASCII file : GENOMIC

```
ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCCAT ATTCATCCCT
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAC TCTTCCGTAT
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAC AAGTAAGCCG
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT
ACCCTTTGTG CC
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA
CGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAC
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC
GAG CAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC CCA
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T
GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA
CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC
TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC
CCCCACTCCT TGCTCCGCTC TCTTTCCTTT TCCCACCTTG CCTCTGGAGC
TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC
TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCCTC
TTCAGGCTTC CCCATTTGCT CCTCTCCCGA AACCCTCCCC TTCCTGTTCC
CCTTTTCGCG CCTTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTTACCTT
TCACCAGCTT TGCTCTCCCT GCTCCCCTCC CCCTTTTGCA CCTTTTCTTT
TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT
CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTTG CATTTTCGGG
TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TTCGGGTGCT
CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TTTTTTTTTT TTTTTTTTTT
TTGGTTTTTC GAGACAGGGT TTCTCTTTGT ATCCCTGGCT GTCCTGGCAC
TCACTCTGTA GACCAGGCTG GCCTCAAACT CAGAAATCTG CCTGCCTCTG
CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC CCCACTGCAG
GCCTTTCTTT TTTCTCCTCT CTGGTCTCCC TAATCCCTTT TCTGCATGTT
AACTCCCCTT TTGGCACCTT TCCTTTACAG GACCCCCTCC CCCTCCCTGT
TTCCCTTCCG GCACCCTTCC TAGCCCTGCT CTGTTCCCTC TCCCTGCTCC
CCTCCCCCTC TTTGCTCGAC TTTTAGCAGC CTTACCTCTC CCTCCTTTCT
GCCCCGTTCC CCTTTTTTGT GCCTTTCCTC CTGGCTCCCC TCCACCTTCC
AGCTCACCTT TTTGTTTGTT TGGTTGTTTG GTTGTTTGGT TTGCTTTTTT
TTTTTTTTTT GCACCTTGTT TTCCAAGATC CCCCTCCCCC TCCGGCTTCC
CCTCTGTGTG CCTTTCCTGT TCCCTCCCCC TCGCTGGCTC CCCCTCCCTT
TCTGCCTTTC CTGTCCCTGC TCCCTTCTCT GCTAACCTTT TAATGCCTTT
CTTTTCTAGA CTCCCCCCTC CAGGCTTGCT GTTTGCTTCT GTGCACTTTT
CCTGACCCTG CTCCCCTTCC CCTCCCAGCT CCCCCCTCTT TTCCCACCTC
CCTTTCTCCA GCCTGTCACC CCTCCTTCTC TCCTCTCTGT TTCTCCCACT
TCCTGCTTCC TTTACCCCTT CCCTCTCCCT ACTCTCCTCC CTGCCTGCTG
GACTTCCTCT CCAGCCGCCC AGTTCCCTGC AGTCCTGGAG TCTTTCCTGC
CTCTCTGTCC ATCACTTCCC CCTAGTTTCA CTTCCCTTTC ACTCTCCCCT
ATGTGTCTCT CTTCCTATCT ATCCCTTCCT TTCTGTCCCC TCTCCTCTGT
CCATCACCTC TCTCCTCCCT TCCCTTTCCT CTCTCTTCCA TTTTCTTCCA
CCTGCTTCTT TACCCTGCCT CTCCCATTGC CCTCTTACCT TTATGCCCAT
TCCATGTCCC CTCTCAATTC CCTGTCCCAT TCTGCTCCCT CACATCTTCC
```

Figure 9

ATTTCCCTCT TTCTCCCTTA GCCTCTTCTT CCTCTTCTCT TGTATCTCCC
TTCCCTTTGC TTCTCCCTCC TCCTTTCCCC TTCCCCTATG CCCTCTACTC
TACTTGATCT TCTCTCCTCT CCACATACCC TTTTTCCTTT CCACCCTCCC
CTTTGTCCCC AGACCCTACA GTATCCTGTG CACAGGAAGT GGGAGGTGCC
ATCAACAACA AGGAGGCAAG AAACAGAGCA AAATCCCAAA ATCAGCAGGA
AAGGCTGGAT GAAAATAAGG CCAGGTTCTG AGGACAGCTG GAATCTAGCC
AAGTGGCTCC TATAACCCTA AGTACCAAGG GAGAAAGTGA TGGTGAAGTT
CTTGATCCTT GCTGCTTCTT TTACATATGT TGGCACATCT TTCTCAAATG
CAGGCCATGC TCCATGCTTG GCGCTTGCTC AGCGTGGTTA AGTAATGGGA
GAATCTGAAA ACTAGGGGCC AGTGGTTTGT TTTGGGGACA AATTAGCACG
TAGTGATATT TCCCCCTAAA AATTATAACA AACAGATTCA TGATTTGAGA
TCCTTCTACA GGTGAGAAGT GGAAAAATTG TCACTATGAA GTTCTTTTTA
GGCTAAAGAT ACTTGGAACC ATAGAAGCGT TGTTAAAATA CTGCTTTCTT
TTGCTAAAAT ATTCTTTCTC ACATATTCAT ATTCTCCAG
GT GTT CCT GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT
AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT
ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA
AAT GCT GAT GAA GAG GTT GCA ATG GAA CAG GAA GAA GAA GAA
GAG GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC
TTC TCA CCT TAG
GCATGCAGGT ACTGGCTTCA CTAACCAACC ATTCCTAACA TATGCCTGTA
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA
TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA
CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTCT TCTTTAGATT
GTAGTGACAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA
GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCCCATATTG
TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT
TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTCTCG
TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT
CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTTCACT
TAGAATTCAA TTCAAATTCT TAATTCAATC TTAATTTTTA GATTTCTTAA
AATGTTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA
GTAACTGGGG GGCTTAGGCA ATCTGTAGGG TTGCGGTATA GCAATAGGGA
GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC
CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC
ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT
ATTTTAGTTT CTCCTTGACA AACAATGACA AGACATAAAA TTGGCAAGAA
AGTCAGGAGT GTATTCTAAT AAGTGTTGCT TATCTCTTAT TTTCTTCTAC
AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTTT
TTTTTTCCCC TTCATTAATT TTCTAGTTTT TAGTAATCCA GAAAATTTGA
TTTTGTTCTA AAGTTCATTA TGCAAAGATG TCACCAACAG ACTTCTGACT
GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTTAAA
AATAAAAGTT TGACTTGCAT AC

Figure 9 (ctd)

Leu-Leu-His-Arg-Tyr-Ser-Leu-Glu-Glu-Ile-Leu-Pro-Tyr-Leu-Gly-Trp-

Val-Phe-Ala-Val-Val-Thr-Thr-Ser-Phe

Figure 10